

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/424,840A

DATE: 06/29/2001

TIME: 13:48:08

Input Set : A:\5649049.app

Output Set: N:\CRF3\06292001\I424840A.raw

3 <110> APPLICANT: BERCHTOLD, Peter
 4 ESCHER, Robert F.A.
 6 <120> TITLE OF INVENTION: Anti-GPIIB/IIIA Recombinant Antibodies
 8 <130> FILE REFERENCE: 100564-09049
 10 <140> CURRENT APPLICATION NUMBER: US 09/424,840A
 11 <141> CURRENT FILING DATE: 1999-12-03
 13 <150> PRIOR APPLICATION NUMBER: DE 19723904.8
 14 <151> PRIOR FILING DATE: 1997-06-06
 16 <150> PRIOR APPLICATION NUMBER: DE 19755227.7
 17 <151> PRIOR FILING DATE: 1997-12-12
 19 <150> PRIOR APPLICATION NUMBER: DE 19820663.1
 20 <151> PRIOR FILING DATE: 1998-05-08
 22 <160> NUMBER OF SEQ ID NOS: 127
 24 <170> SOFTWARE: PatentIn Ver. 2.1

26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 357
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (1)..(357)
 35 <400> SEQUENCE: 1

36 cag gtg aaa ctg ctg gag tcg ggc cca gga ctg gtg aag cct tcg gag 48
 37 Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 38 1 5 10 15
 40 acc ctg tcc ctg aac tgc act gtc tct ggt cgc tcc atc agt ggt tac 96
 41 Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr
 42 20 25 30
 44 tct tgg aga tgg atc cgg cag tct cca ggg aag gga cta gag tgg att 144
 45 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 46 35 40 45
 48 ggg gat atc tct tat agt ggg agt acc aag tac aaa ccc tcc ctg agg 192
 49 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
 50 50 55 60
 52 agt cga gtc acc ctg tca gta gac acg tcc aag aac cag ttc tcc ctg 240
 53 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 54 65 70 75 80
 56 aag ctg aat tcg gtg acc gct gcg gac acg gcc gtc tat tac tgt gcg 288
 57 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 58 85 90 95
 60 cga gtc ttg ccc ttt gac ccg atc tcg atg gac gtc tgg ggc aaa ggg 336
 61 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly
 62 100 105 110
 64 acc acg gtc acc gtc tcc tca 357
 65 Thr Thr Val Thr Val Ser Ser
 66 115
 69 <210> SEQ ID NO: 2

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70 <211> LENGTH: 119

71 <212> TYPE: PRT

72 <213> ORGANISM: Homo sapiens

74 <400> SEQUENCE: 2

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75 Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
76   1           5           10           15
78 Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr
79           20           25           30
81 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
82           35           40           45
84 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
85           50           55           60
87 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
88   65           70           75           80
90 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
91           85           90           95
93 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly
94           100          105          110
96 Thr Thr Val Thr Val Ser Ser
97           115

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101 <210> SEQ ID NO: 3

102 <211> LENGTH: 333

103 <212> TYPE: DNA

104 <213> ORGANISM: Homo sapiens

106 <220> FEATURE:

107 <221> NAME/KEY: CDS

108 <222> LOCATION: (1)..(333)

110 <400> SEQUENCE: 3

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111 gtg gtg act cag cca ccc tca gcg tct ggg acc ccc ggg cag tgg gtc 48
112 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Trp Val
113   1           5           10           15
115 acc atc tct tgt tct ggg agc agc tcc aac atc aga agt aat cct gtt 96
116 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
117           20           25           30
119 agc tgg tat cac cag gtc cca ggc acg gcc ccc aaa ctc ctc atc ttt 144
120 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
121           35           40           45
123 ggt agt cat cag cgg ccc tca ggg gtc cct gac cga ttc tct ggc tcc 192
124 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
125           50           55           60
127 aag tcg ggc acc tcc gcc tcc ctg gcc atc cgt ggg ctc caa tct ggg 240
128 Lys Ser Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
129   65           70           75           80
131 gat gct ggt gac tat tac tgt gca aca tgg gat gac ggc ctc aat ggt 288
132 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
133           85           90           95
135 ccg gtg ttc ggc gga ggg acc aag ctg acc gtc cta agt cag ccc 333
136 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
137           100          105          110

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140 <210> SEQ ID NO: 4
141 <211> LENGTH: 111
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens
145 <400> SEQUENCE: 4
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147   1          5          10          15
149 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
150   20          25          30
152 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
153   35          40          45
155 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
156   50          55          60
158 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
159   65          70          75          80
161 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
162   85          90          95
164 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
165   100         105         110
169 <210> SEQ ID NO: 5
170 <211> LENGTH: 369
171 <212> TYPE: DNA
172 <213> ORGANISM: Homo sapiens
174 <220> FEATURE:
175 <221> NAME/KEY: CDS
176 <222> LOCATION: (1)..(369)
178 <400> SEQUENCE: 5
179 `cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag cct ggg agg      48
180 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
181   1          5          10          15
183 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tat      96
184 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
185   20          25          30
187 gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg      144
188 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
189   35          40          45
191 gca gtt ata tca tat gat gga agc aat aaa tac tac gca gac tcc gtg      192
192 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
193   50          55          60
195 aag ggc cga ttc gcc atc tcc aga gac aat tcc aag aac acg ctg tat      240
196 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
197   65          70          75          80
199 ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt      288
200 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
201   85          90          95
203 gcg aga gcg ctg ggg agc tgg ggg ggt tgg gac cac tac atg gac gtc      336
204 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
205   100         105         110
207 tgg ggc aaa ggg acc acg gtc acc gtc tcc tca      369

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208 Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
209      115      120
212 <210> SEQ ID NO: 6
213 <211> LENGTH: 123
214 <212> TYPE: PRT
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 6
218 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
219      1      5      10      15
221 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
222      20      25      30
224 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
225      35      40      45
227 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
228      50      55      60
230 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
231      65      70      75      80
233 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
234      85      90      95
236 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
237      100     105     110
239 Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
240      115     120
244 <210> SEQ ID NO: 7
245 <211> LENGTH: 333
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapiens
249 <220> FEATURE:
250 <221> NAME/KEY: CDS
251 <222> LOCATION: (1)..(333)
253 <400> SEQUENCE: 7
254 gtg gtg act cag cca ccc tca gcg tct ggg acc ccc ggg cag agg gtc      48
255 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
256      1      5      10      15
258 acc atc tct tgt tct gga agc agc tcc aac atc gga agt aat act gta      96
259 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
260      20      25      30
262 aac tgg tac cag cag ctc cca gga acg gcc ccc aaa ctc ctc atc tat      144
263 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
264      35      40      45
266 agt aat aat cag cgg ccc tca ggg gtc cct gac cga ttc tct ggc tcc      192
267 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
268      50      55      60
270 aag tct ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag tct gag      240
271 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
272      65      70      75      80
274 gat gag gct gat tat tac tgt gca gca tgg gat gac agc ctg aat ggt      288
275 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
276      85      90      95

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278 tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc 333
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280      100      105      110
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284 <211> LENGTH: 111
285 <212> TYPE: PRT
286 <213> ORGANISM: Homo sapiens
288 <400> SEQUENCE: 8
289 Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
290      1      5      10      15
292 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
293      20      25      30
295 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
296      35      40      45
298 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
299      50      55      60
301 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
302      65      70      75      80
304 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
305      85      90      95
307 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
308      100      105      110
312 <210> SEQ ID NO: 9
313 <211> LENGTH: 369
314 <212> TYPE: DNA
315 <213> ORGANISM: Homo sapiens
317 <220> FEATURE:
318 <221> NAME/KEY: CDS
319 <222> LOCATION: (1)..(369)
321 <400> SEQUENCE: 9
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323 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
324      1      5      10      15
326 tcc ctg aga ctc tct tgt gca gcc tct gga ttt acg ttt gac aac ttt 96
327 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe
328      20      25      30
330 gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc 144
331 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
332      35      40      45
334 tca ggc att agt ggt ggt ggt ctt ttg aca cac tac gca gac tcc gtg 192
335 Ser Gly Ile Ser Gly Gly Gly Leu Leu Thr His Tyr Ala Asp Ser Val
336      50      55      60
338 aag ggc cgg ttc acc atc tcc aga aac aat tcc agg aac act gta tac 240
339 Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ser Arg Asn Thr Val Tyr
340      65      70      75      80
342 cta caa atg aac agc ctg aga gcc gaa gac acg gcc gtg tat tat tgt 288
343 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
344      85      90      95
346 gtg aga gat ctg ggc tat aga gta ctt tcg act ttt act ttt gat atc 336

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VERIFICATION SUMMARY

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